



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:05 PM UTC

PDB ID : 1P31 / pdb_00001p31
Title : Crystal Structure of UDP-N-acetylmuramic acid:L-alanine Ligase (MurC) from Haemophilus influenzae
Authors : Mol, C.D.; Brooun, A.; Dougan, D.R.; Hilgers, M.T.; Tari, L.W.; Wijnands, R.A.; Knuth, M.W.; McRee, D.E.; Swanson, R.V.
Deposited on : 2003-04-16
Resolution : 1.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

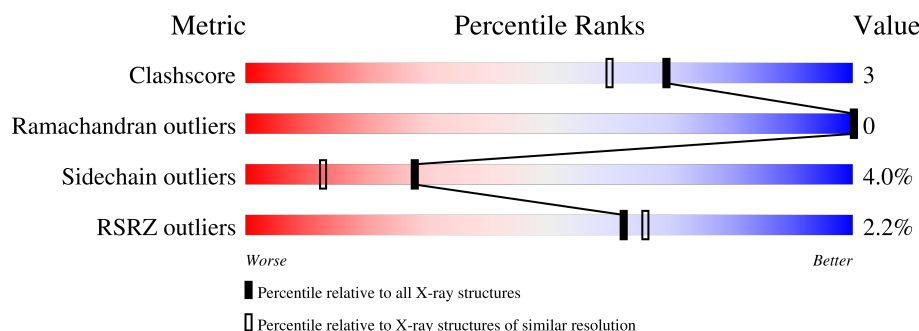
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	475	4% 85% 12% .
1	B	475	% 88% 9% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7928 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called UDP-N-acetylmuramate--alanine ligase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	Se	0	1	0
			3554	2238	623	676	3	14			
1	B	465	Total	C	N	O	S	Se	0	4	0
			3582	2257	629	679	3	14			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P45066
A	15	MSE	MET	modified residue	UNP P45066
A	31	MSE	MET	modified residue	UNP P45066
A	110	MSE	MET	modified residue	UNP P45066
A	115	MSE	MET	modified residue	UNP P45066
A	135	MSE	MET	modified residue	UNP P45066
A	138	MSE	MET	modified residue	UNP P45066
A	187	MSE	MET	modified residue	UNP P45066
A	194	MSE	MET	modified residue	UNP P45066
A	199	MSE	MET	modified residue	UNP P45066
A	209	MSE	MET	modified residue	UNP P45066
A	228	MSE	MET	modified residue	UNP P45066
A	236	MSE	MET	modified residue	UNP P45066
A	371	MSE	MET	modified residue	UNP P45066
A	400	MSE	MET	modified residue	UNP P45066
B	1	MSE	MET	modified residue	UNP P45066
B	15	MSE	MET	modified residue	UNP P45066
B	31	MSE	MET	modified residue	UNP P45066
B	110	MSE	MET	modified residue	UNP P45066
B	115	MSE	MET	modified residue	UNP P45066
B	135	MSE	MET	modified residue	UNP P45066
B	138	MSE	MET	modified residue	UNP P45066
B	187	MSE	MET	modified residue	UNP P45066
B	194	MSE	MET	modified residue	UNP P45066
B	199	MSE	MET	modified residue	UNP P45066

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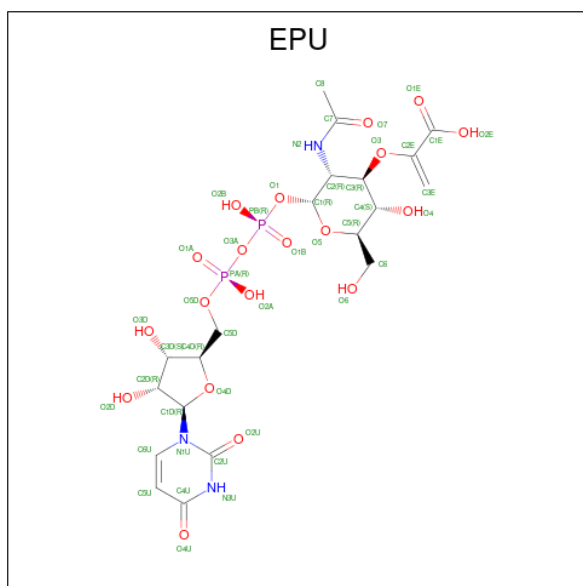
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Chain	Residue	Modelled	Actual	Comment	Reference
B	209	MSE	MET	modified residue	UNP P45066
B	228	MSE	MET	modified residue	UNP P45066
B	236	MSE	MET	modified residue	UNP P45066
B	371	MSE	MET	modified residue	UNP P45066
B	400	MSE	MET	modified residue	UNP P45066

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	B	2	Total Mg 2 2	0	0

- Molecule 3 is URIDINE-DIPHOSPHATE-2(N-ACETYLGUCOSAMINYL) BUTYRIC ACID (CCD ID: EPU) (formula: C₂₀H₂₉N₃O₁₉P₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 44 20 3 19 2	0	0
3	B	1	Total C N O P 44 20 3 19 2	0	0

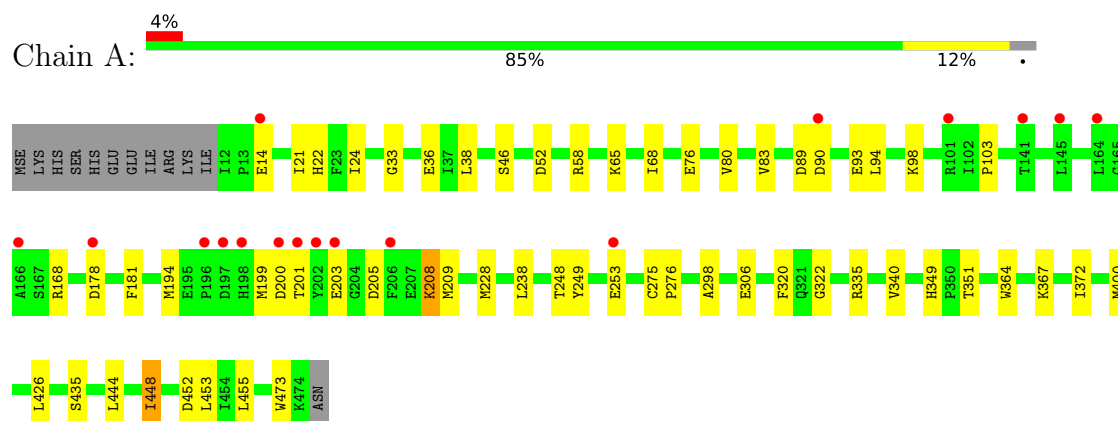
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	335	Total 335	O 335	0	0
4	B	365	Total 365	O 365	0	0

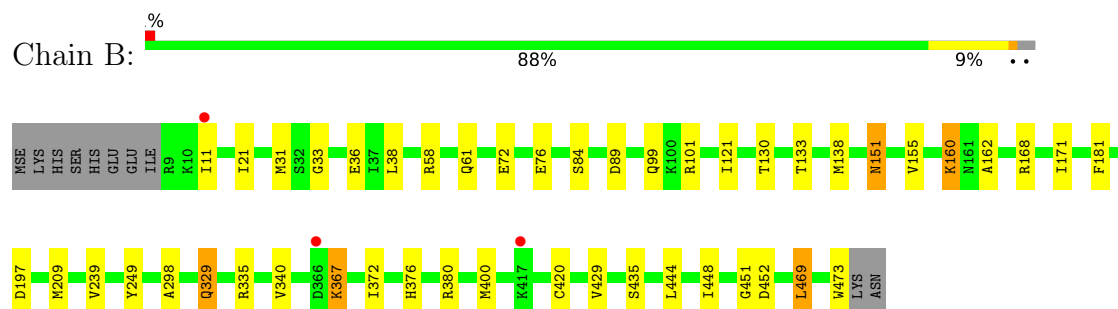
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: UDP-N-acetylmuramate--alanine ligase



- Molecule 1: UDP-N-acetylmuramate--alanine ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.52Å 92.27Å 118.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.85 25.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	89.8 (25.00-1.85) 89.7 (25.00-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.169 , 0.208 0.173 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	19.3	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7928	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPU, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	1/3607 (0.0%)	0.80	0/4859
1	B	0.49	1/3646 (0.0%)	0.79	0/4910
All	All	0.48	2/7253 (0.0%)	0.80	0/9769

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	239	VAL	CA-CB	5.50	1.56	1.54
1	A	400	MSE	SE-CE	-5.24	1.79	1.95

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

CLOSE-CONTACTS INFOmissingINFO

5.2 Torsion angles [i](#)

5.2.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	462/475 (97%)	458 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	467/475 (98%)	463 (99%)	4 (1%)	0	100	100
All	All	929/950 (98%)	921 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.2.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	376/372 (101%)	362 (96%)	14 (4%)	30	15
1	B	381/372 (102%)	364 (96%)	17 (4%)	24	10
All	All	757/744 (102%)	726 (96%)	31 (4%)	28	12

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLU
1	A	65	LYS
1	A	76	GLU
1	A	89	ASP
1	A	90	ASP
1	A	98	LYS
1	A	168	ARG
1	A	181	PHE
1	A	200	ASP
1	A	208	LYS
1	A	253	GLU
1	A	426	LEU
1	A	448	ILE
1	A	455	LEU
1	B	11	ILE
1	B	61	GLN
1	B	72	GLU
1	B	76	GLU

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Mol	Chain	Res	Type
1	B	89	ASP
1	B	99	GLN
1	B	101	ARG
1	B	151	ASN
1	B	160	LYS
1	B	168	ARG
1	B	181	PHE
1	B	329	GLN
1	B	367	LYS
1	B	429[A]	VAL
1	B	429[B]	VAL
1	B	448	ILE
1	B	469	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	106	GLN
1	A	268	GLN
1	A	278	ASN
1	A	286	ASN
1	A	439	GLN
1	A	446	GLN
1	B	61	GLN
1	B	99	GLN
1	B	106	GLN
1	B	142	GLN
1	B	151	ASN
1	B	163	HIS
1	B	254	GLN
1	B	282	ASN
1	B	376	HIS
1	B	394	GLN

5.2.3 RNA ⓘ

There are no RNA molecules in this entry.

5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.4 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.5 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EPU	B	602	2	45,46,46	1.22	6 (13%)	63,69,69	1.60	9 (14%)
3	EPU	A	598	2	45,46,46	1.31	6 (13%)	63,69,69	1.46	9 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EPU	B	602	2	-	12/32/71/71	0/3/3/3
3	EPU	A	598	2	-	10/32/71/71	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	EPU	O3-C2E	3.41	1.47	1.36
3	A	598	EPU	O3-C2E	3.36	1.46	1.36
3	A	598	EPU	C7-N2	3.35	1.45	1.34
3	B	602	EPU	C7-N2	3.10	1.44	1.34
3	A	598	EPU	C2E-C1E	-2.76	1.46	1.49
3	B	602	EPU	C4U-N3U	-2.38	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	598	EPU	C2U-N3U	-2.35	1.33	1.38
3	B	602	EPU	C2E-C1E	-2.35	1.47	1.49
3	A	598	EPU	C4U-N3U	-2.32	1.34	1.38
3	B	602	EPU	C2U-N1U	2.16	1.41	1.38
3	A	598	EPU	PA-O3A	2.13	1.61	1.59
3	B	602	EPU	C6U-C5U	2.04	1.39	1.35

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	EPU	C4U-N3U-C2U	-5.11	120.26	126.61
3	A	598	EPU	C5U-C4U-N3U	4.37	120.92	114.80
3	A	598	EPU	C4U-N3U-C2U	-4.30	121.28	126.61
3	B	602	EPU	C5U-C4U-N3U	4.22	120.71	114.80
3	B	602	EPU	N3U-C2U-N1U	4.14	120.28	114.89
3	B	602	EPU	O3-C3-C2	3.64	114.64	107.92
3	B	602	EPU	O2E-C1E-C2E	3.58	120.02	113.91
3	B	602	EPU	O3-C3-C4	3.45	115.69	107.76
3	A	598	EPU	O3-C3-C4	3.43	115.63	107.76
3	A	598	EPU	O2E-C1E-C2E	3.42	119.73	113.91
3	A	598	EPU	N3U-C2U-N1U	3.31	119.21	114.89
3	A	598	EPU	O4U-C4U-C5U	-3.10	119.82	125.16
3	B	602	EPU	O4U-C4U-C5U	-2.84	120.26	125.16
3	A	598	EPU	O3-C3-C2	2.72	112.95	107.92
3	B	602	EPU	O2U-C2U-N1U	-2.46	119.60	122.80
3	B	602	EPU	C3E-C2E-C1E	-2.05	118.93	122.73
3	A	598	EPU	O1E-C1E-C2E	-2.04	118.71	121.79
3	A	598	EPU	C8-C7-N2	2.01	119.45	116.12

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	598	EPU	C1-O1-PB-O3A
3	A	598	EPU	C1-O1-PB-O2B
3	A	598	EPU	O1E-C1E-C2E-C3E
3	A	598	EPU	O2E-C1E-C2E-C3E
3	B	602	EPU	C1-O1-PB-O3A
3	B	602	EPU	C1-O1-PB-O2B
3	B	602	EPU	O1E-C1E-C2E-C3E
3	B	602	EPU	O2E-C1E-C2E-C3E
3	A	598	EPU	C4-C3-O3-C2E

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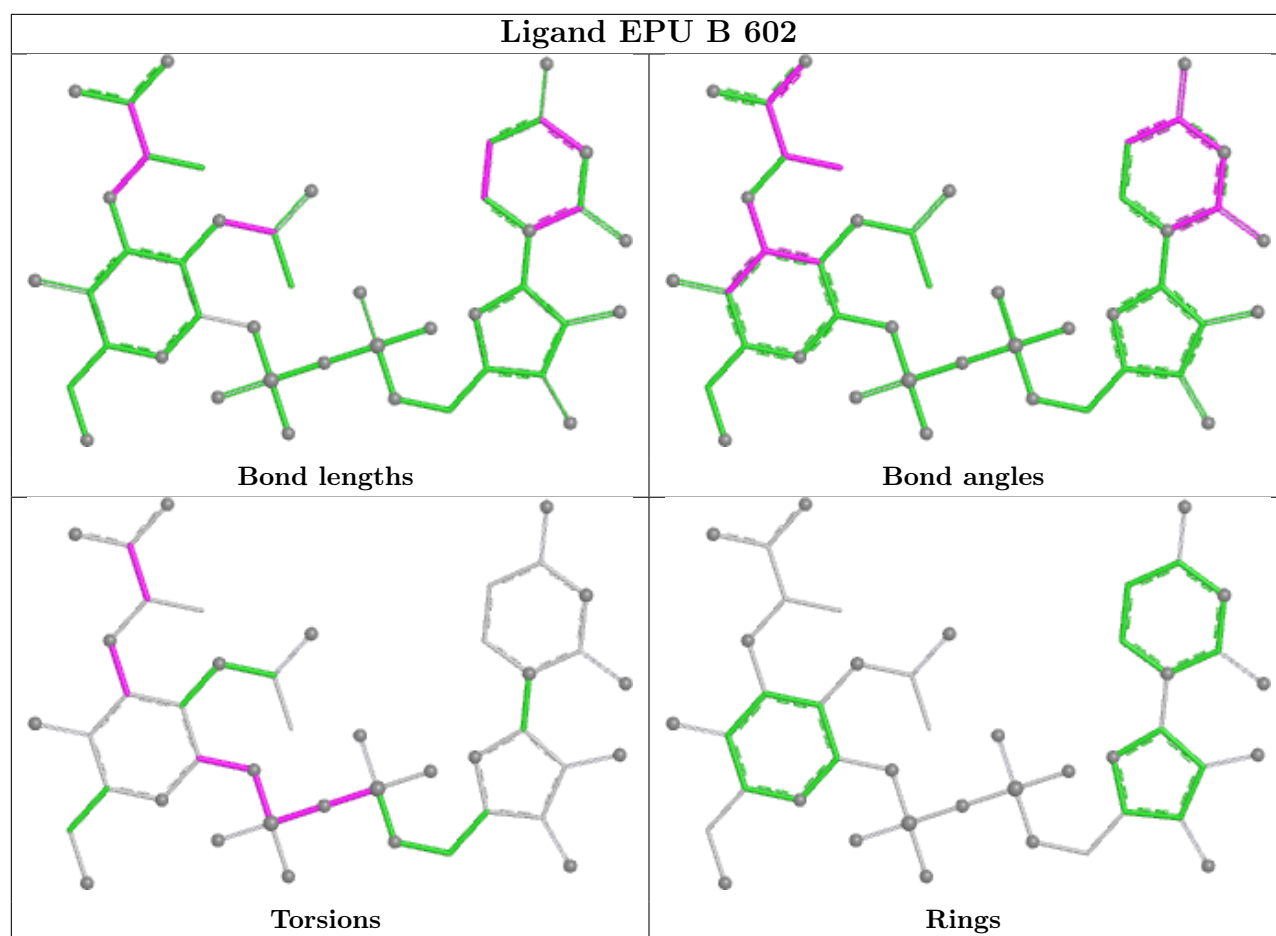
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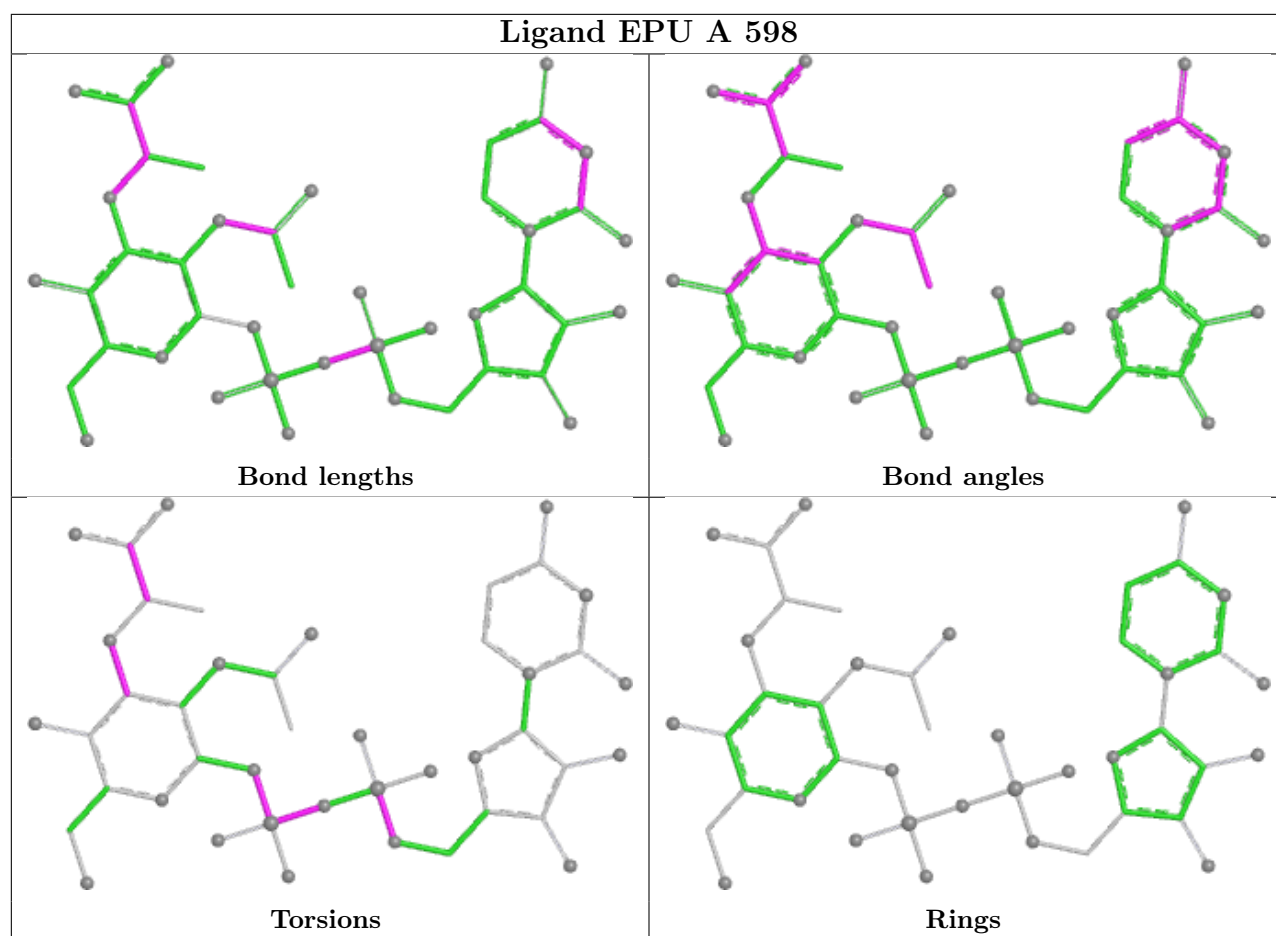
Mol	Chain	Res	Type	Atoms
3	B	602	EPU	C2-C3-O3-C2E
3	A	598	EPU	O1E-C1E-C2E-O3
3	B	602	EPU	O1E-C1E-C2E-O3
3	A	598	EPU	PA-O3A-PB-O1
3	B	602	EPU	PA-O3A-PB-O1
3	B	602	EPU	C4-C3-O3-C2E
3	A	598	EPU	C5D-O5D-PA-O3A
3	A	598	EPU	C2-C3-O3-C2E
3	B	602	EPU	O5-C1-O1-PB
3	A	598	EPU	O2E-C1E-C2E-O3
3	B	602	EPU	O2E-C1E-C2E-O3
3	B	602	EPU	C1-O1-PB-O1B
3	B	602	EPU	PB-O3A-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.6 Other polymers [i](#)

There are no such residues in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	449/475 (94%)	0.19	17 (3%) 44 48	6, 11, 17, 33	1 (0%)
1	B	451/475 (94%)	-0.17	3 (0%) 84 87	6, 10, 17, 38	4 (0%)
All	All	900/950 (94%)	0.01	20 (2%) 62 66	6, 11, 17, 38	5 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	203	GLU	4.1
1	A	201	THR	3.9
1	A	253	GLU	3.9
1	B	11	ILE	3.8
1	A	200	ASP	3.4
1	A	196	PRO	3.2
1	A	101	ARG	3.2
1	A	197	ASP	3.2
1	A	164	LEU	3.0
1	A	198	HIS	2.9
1	A	14	GLU	2.8
1	B	366	ASP	2.7
1	A	178	ASP	2.6
1	A	141	THR	2.5
1	B	417	LYS	2.3
1	A	202	TYR	2.2
1	A	166	ALA	2.2
1	A	145	LEU	2.1
1	A	90	ASP	2.1
1	A	206	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

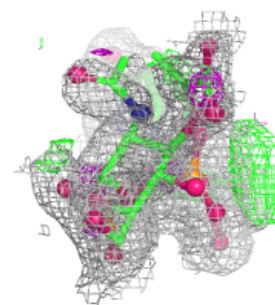
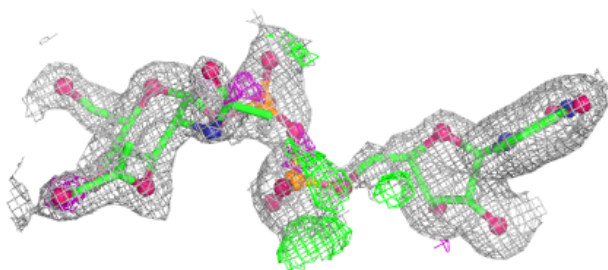
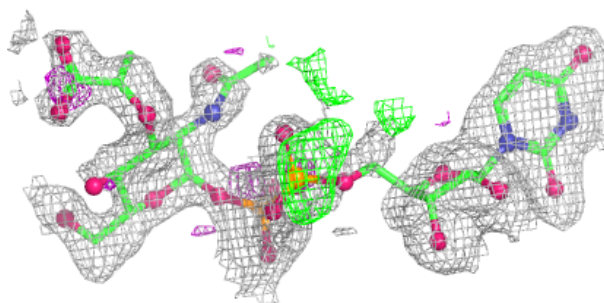
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EPU	A	598	44/44	0.89	0.12	24,36,43,43	0
2	MG	A	776	1/1	0.91	0.10	42,42,42,42	0
2	MG	B	601	1/1	0.94	0.05	17,17,17,17	0
2	MG	B	710	1/1	0.94	0.07	42,42,42,42	0
3	EPU	B	602	44/44	0.96	0.07	18,20,28,31	0
2	MG	A	611	1/1	0.98	0.03	30,30,30,30	0

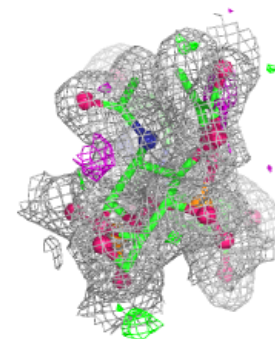
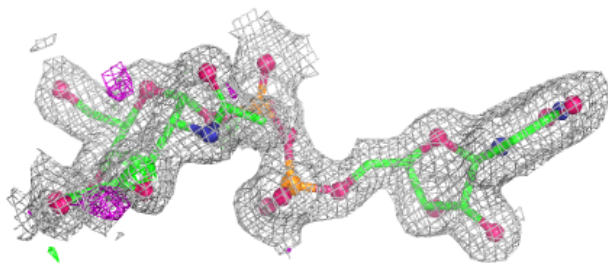
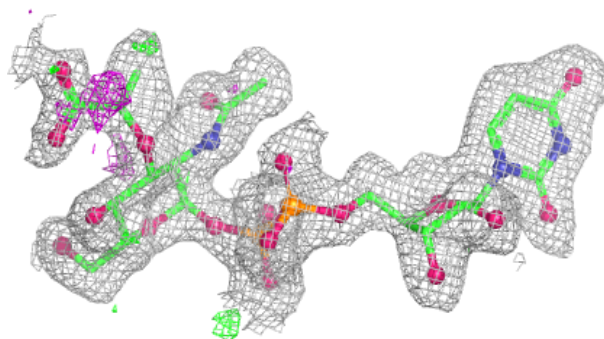
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around EPU A 598:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around EPU B 602:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.